X-15984.ST25.txt

SEQUENCE LISTING

<110> Wolfgang Glaesner, et al.

<120> GLP-1 Analog Fusion Proteins

<130> X-15984

<150> 60/477880
<151> 2003-06-12

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<170> PatentIn version 3.3

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<400> 1

His Xaa Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu
1   5   10   15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Gly Gly
            20   25   30

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His Xaa Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu
1   5   10   15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Lys Asn Gly Gly Gly
            20   25   30

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His Xaa Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu
1               5                   10                  15


Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Gly Pro
            20                  25                  30


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His Xaa Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu
1               5                   10                  15


Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Lys Asn Gly Gly Pro
            20                  25                  30


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His Xaa Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu
1   5   10   15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Gly
            20   25   30

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His Xaa Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu
1   5   10   15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Lys Asn Gly Gly
            20   25   30

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<223>   Xaa at position 17 is Phe, Val, or Ala

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<223>   Xaa at position 18 is Leu, Glu, or Ala

<220>
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Ala Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Xaa
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Xaa Xaa Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            20   25   30

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        35   40   45

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
    50   55   60

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Xaa
65   70   75   80

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
            85   90   95

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
            100   105   110

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        115   120   125

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
    130   135   140

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
145   150   155   160

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            165   170   175

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
            180   185   190

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
        195   200   205

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    210   215   220

Ser Leu Ser Leu Gly Xaa

225   230

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Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1   5   10   15

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<400>   9

His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
1   5   10   15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
            20   25   30

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His Gly Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Glu
1   5   10   15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly Gly
            20   25   30

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
            35   40   45

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Glu Ser
        50   55   60

Lys Tyr Gly Pro Pro Cys Pro
65   70

<210>   11

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Trp Leu Val Lys Gly Arg Gly Gly Gly
1                   5


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<400>    12

Trp Leu Val Lys Gly Gly Gly
1                   5


<210>    13
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<400>    13

Trp Leu Lys Asn Gly Gly Gly
1                   5


<210>    14
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<400>    14

Trp Leu Val Lys Gly Gly Pro
1                   5


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Trp Leu Lys Asn Gly Gly Pro
1   5

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Trp Leu Val Lys Gly Gly
1   5

<210> 17
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Trp Leu Lys Asn Gly Gly
1   5

<210> 18
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<400> 18

Pro Pro Cys Pro Ser Cys
1   5

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Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1   5   10   15

Ser Gly Gly Gly Gly Ser
            20

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<400> 20

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tctggtggcg gtggcagcgc tgagtccaaa tatggtcccc catgcccacc ctgcccagca   180

cctgaggccg ccggggggacc atcagtcttc ctgttccccc caaaacccaa ggacactctc   240

atgatctccc ggacccctga ggtcacgtgc gtggtggtgg acgtgagcca ggaagacccc   300

gaggtccagt tcaactggta cgtggatggc gtggaggtgc ataatgccaa gacaaagccg   360

cgggaggagc agttcaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag   420

gactggctga cggcaagga gtacaagtgc aaggtctcca caaaggcct cccgtcctcc   480

atcgagaaaa ccatctccaa agccaaaggg cagccccgag agccacaggt gtacaccctg   540

ccccatccc aggaggagat gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc   600

ttctacccca gcgacatcgc cgtggagtgg gaaagcaatg ggcagccgga gaacaactac   660

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1               5                   10                  15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            20                  25                  30
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